

## Species *Salsuginivita brisbanensis*<sup>Ts</sup>

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### Etymology

[bris.ban.en'sis] N.L. fem. adj. *brisbanensis*, of or belonging to Brisbane

### Nomenclatural type

[NCBI Assembly: GCA\\_038144975.1](#)<sup>Ts</sup>

### Description

Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Mucin, Starch) as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Capable of nitrate uptake (NRT2), phosphorus uptake and regulation (pho, pst), polyphosphate accumulation (ppk1) and noted absence of osmoregulation genes. Based on the genome reporting standards for MAGs, the estimated completeness was 98.63%, contamination 0%, and the presence of the 16S (1,555 bp), and 23S (2, 882bp) rRNA gene and 46 tRNAs. Type genome is defined as "high-quality" draft MAG, with genome size of 2.5Mbps.

### Classification

*Bacteria* » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Opitutaceae* » *Salsuginivita* » *Salsuginivita brisbanensis*<sup>Ts</sup>

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46749>

## References

1. Prabhu et al. (2024). Machine learning and metagenomics identifies uncharacterized taxa inferred to drive biogeochemical cycles in a subtropical hypereutrophic estuary. *ISME Communications*.  
[DOI:10.1093/ismeco/ycae067](https://doi.org/10.1093/ismeco/ycae067)